=> D BIB ABS L28 1

L28 ANSWER 1 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:772855 HCAPLUS
DN 133:349119
TI Phage inactivation by expressed epitopes recognized by natural antibodies
IN Wolff, Jon A.
PA Mirus Corporation, USA
SO PCT Int. Appl., 87 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000065350	A1	20001102	WO 2000-US11270	20000427

W: JP
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRAI US 1999-131151 19990427
US 1999-139431 19990607

AB The author discloses in vivo and in vitro phage peptide display methods for the identification and selection of peptides and peptide assocd. factors with desired properties (e.g., tissue targeting specificity, stability against inactivation, etc.). In one example, the author characterizes phage sensitivity to complement-mediated inactivation to natural antibodies binding to the C-terminal portion of the 10B coat protein. In a second example, muteins of the coat protein exhibiting resistance to complement-mediated inactivation are shown to be due to binding by C-reactive protein. The present invention further provides methods and compns. for the isolation and identification of peptide-specific antibodies.

RE.CNT 4
RE
(1) Lorenzi; Immunotechnology 1999, V4, P267 HCAPLUS
(2) Merril; US 5811093 A 1998 HCAPLUS
(3) Merril; Proc Natl Acad Sci USA 1996, V93, P3188 HCAPLUS
(4) Ruoslahti; US 5622699 A 1997 HCAPLUS

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=> D BIB ABS L28 2

L28  ANSWER 2 OF 35  HCAPLUS  COPYRIGHT 2001 ACS
AN   2000:688462  HCAPLUS
DN   133:265653
TI   Protein isolation and analysis
IN   Carr, Francis J.
PA   Biovation Limited, UK
SO   PCT Int. Appl., 53 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.         KIND  DATE          APPLICATION NO.  DATE
     ----------------   ----  --------      ---------------  --------
PI   WO 2000057183      A1    20000928      WO 2000-GB1015   20000317
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR,
             CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
             ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
             LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,
             SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA,
             ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
             DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
             CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI GB 1999-6551      19990323
     GB 1999-7057      19990329
     GB 1999-7641      19990406
     GB 1999-14874     19990628
     GB 1999-15363     19990702
     GB 1999-15677     19990706
     GB 1999-16511     19990714
     GB 1999-20503     19990831
     GB 1999-22285     19990921
AB   Novel methods for the identification and/or sequencing of
     proteins are provided.  These methods are particularly suited to screening
     antibody libraries and in preferred embodiments make use of mass
     spectrometry techniques for direct or indirect sequencing.
RE.CNT  10
RE
(1) Cao, P; JOURNAL OF THE AMERICAN SOCIETY FOR MASS SPECTROMETRY 1998, V9(10),
    P1081 HCAPLUS
(2) Ciba Geigy Ag; WO 9516209 A 1995 HCAPLUS
(4) Ducret, A; PROTEIN SCIENCE 1998, V7, P706 HCAPLUS
(7) Nikolaiev, V; PEPTIDE RESEARCH 1993, V6(3), P161 HCAPLUS
(8) Protein Eng Corp; WO 9215679 A 1992 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT
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=> D BIB ABS L28 3

L28 ANSWER 3 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:531256 HCAPLUS
DN 133:251022
TI Utilisation of bacteriophage display libraries to identify peptide sequences recognised by Equine herpesvirus type 1 specific equine sera
AU Birch-Machin, I.; Ryder, S.; Taylor, L.; Iniguez, P.; Marault, M.; Ceglie, L.; Zientara, S.; Cruciere, C.; Cancellotti, F.; Koptopoulos, G.; Mumford, J.; Binns, M.; Davis-Poynter, N.; Hannant, D.
CS Animal Health Trust, Centre for Preventive Medicine, Newmarket, CB8 7UU, UK
SO J. Virol. Methods (2000), 88(1), 89-104
CODEN: JVMEDH; ISSN: 0166-0934
PB Elsevier Science B.V.
DT Journal
LA English
AB Three filamentous phage random peptide display libraries were used in biopanning expts. with purified IgG from the serum of a gnotobiotic foal infected with equine herpesvirus-1 (EHV-1) to enrich for epitopes binding to anti-EHV-1 antibodies. The sequences of the amino acids displayed were aligned with protein sequences of EHV-1, thereby identifying a no. of potential antibody binding regions. Presumptive epitopes were identified within the proteins encoded by genes 7 (DNA helicase/primase complex protein), 11 (tegument protein), 16 (glycoprotein C), 41 (integral membrane protein), 70 (glycoprotein G), 71 (envelope glycoprotein gp300), and 74 (glycoprotein E). Two groups of sequences, which aligned with either glycoprotein C (gC) or glycoprotein E (gE), identified type-specific epitopes which could be used to distinguish between sera from horses infected with either EHV-1 or EHV-4 in an ELISA using either the phage displaying the peptide or synthetic peptides as antigen. The gC epitope had been previously identified as an immunogenic region by conventional monoclonal antibody screening whereas the gE antibody binding region had not been previously identified. This demonstrates that screening of phage display peptide libraries with post-infection polyclonal sera is a suitable method for identifying diagnostic antigens for viral infections such as EHV-1.
RE.CNT 36
RE
(1) Allen, G; J Virol 1987, V61, P2454 HCAPLUS
(4) Ben Porat, T; Virology 1986, V154, P325 HCAPLUS
(5) Chen, Y; Proc Natl Acad Sci USA 1996, V93, P1997 HCAPLUS
(7) Crabb, B; J Virol 1993, V67, P6332 HCAPLUS
(8) Crabb, B; Vet Microbiol 1995, V46, P181 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> D BIB ABS L28 4

L28 ANSWER 4 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:723209 HCAPLUS
DN 131:318562
TI Novel method for the identification of clones conferring a desired biological property from an expression library
IN Cahill, Dolores; Bussow, Konrad; Walter, Gerald; Lehrach, Hans
PA Max-Planck-Gesellschaft zur Forderung der Wissenschaften e.V., Germany
SO PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9957311	A2	19991111	WO 1999-EP2963	19990430
	WO 9957311	A3	20000330		
	W: AU, CA, JP, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9941369	A1	19991123	AU 1999-41369	19990430
PRAI	US 1998-70590		19980430		
	WO 1999-EP2963		19990430		

AB The present invention relates to a novel method for the identification and/or characterization of clones conferring a desired biol. property from an expression library. The method of the invention comprises the step of analyzing for the expression of at least one (poly)peptide, such as a tag expressed as a fusion protein, together with a recombinant insert of a clone of said expression library, wherein the clones of said expression library are arranged in arrayed form. Said (poly)peptide may be fused N-terminally or C-terminally to said insert. The method of the invention further comprises the steps of contacting a ligand specifically interacting with a (poly)peptide expressed by the insert of a clone conferring said desired biol. property with a first replica of said library of clones in arrayed form and analyzing said library of clones for the occurrence of an interaction, and/or carrying out a hybridization or an oligonucleotide fingerprint with a nucleic acid probe specific for the insert of a clone conferring said desired biol. property with a second replica of said library of clones arranged in arrayed form and analyzing said library of clones for the occurrence of a specific hybridization. Finally, the method of the invention requires the identification of clones wherein an expression of the at least one (poly)peptide in step (a) and/or an interaction in step (b) and/or a hybridization or an oligonucleotide fingerprint in step (c) can be detected. The present invention also relates to a kit useful for carrying out the method of the invention.

=> D BIB ABS L28 5

L28 ANSWER 5 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:524383 HCAPLUS
DN 131:268625
TI Single amino acid substitutions globally suppress the folding defects of temperature-sensitive folding mutants of phage P22 coat protein
AU Aramli, Lili A.; Teschke, Carolyn M.
CS Department of Molecular and Cell Biology, University of Connecticut, Storrs, CT, 06269-3125, USA
SO J. Biol. Chem. (1999), 274(32), 22217-22224
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The amino acid sequence of a polypeptide defines both the folding pathway and the final three-dimensional structure of a protein. Eighteen amino acid substitutions have been identified in bacteriophage P22 coat protein that are defective in folding and cause their folding intermediates to be substrates for GroEL and GroES. These temp.-sensitive folding (tsf) substitutions identify amino acids that are crit. for directing the folding of coat protein. Addnl. amino acid residues that are crit. to the folding process of P22 coat protein were identified by isolating second site suppressors of the tsf coat proteins. Suppressor substitutions isolated from the phage carrying the tsf coat protein substitutions included global suppressors, which are substitutions capable of alleviating the folding defects of numerous tsf coat protein mutants. In addn., potential global and site-specific suppressors were isolated, as well as a group of same site amino acid substitutions that had a less severe phenotype than the tsf parent. The global suppressors were located at positions 163, 166, and 170 in the coat protein sequence and were 8-190 amino acid residues away from the tsf parent. Although the folding of coat proteins with tsf amino acid substitutions was improved by the global suppressor substitutions, GroEL remained necessary for folding. Therefore, we believe that the global suppressor sites identify a region that is crit. to the folding of coat protein.
RE.CNT 69
RE
(1) Anfinsen, C; Science 1973, V181, P223 HCAPLUS
(3) Betts, S; Adv Protein Chem 1997, V50, P243 HCAPLUS
(5) Bottema, C; Methods Enzymol 1993, V218, P388 HCAPLUS
(6) Bowie, J; Science 1990, V247, P1306 HCAPLUS
(7) Chothia, C; Annu Rev Biochem 1984, V53, P537 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> D BIB ABS L28 6

L28 ANSWER 6 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:449827 HCAPLUS
DN 131:224196
TI Sequence analysis of the Mycoplasma arthritidis bacteriophage MAV1 genome identifies the putative virulence factor
AU Voelker, LeRoy L.; Dybvig, Kevin
CS Department of Comparative Medicine, University of Alabama at Birmingham, Birmingham, AL, USA
SO Gene (1999), 233(1-2), 101-107
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB The bacteriophage MAV1 is required for the development of arthritis in rats after infection with its host Mycoplasma arthritidis. To identify the phage-encoded virulence factor for this arthritis, the complete nucleotide sequence of MAV1 was detd. The linear double-stranded genome of MAV1 is 15,644 bp and contains 15 ORFs . Putative protein products from these ORFs were identified by comparison of the deduced amino acid sequences to known proteins and comprise DNA replication, restriction-modification, structural, regulatory, and integration/excision proteins. Eight putative promoters were identified; four of these would produce polycistronic transcripts. Translation of each ORF appears to be initiated independently, with each having its own RBS. A single ORF, vir, was identified on the minus strand of the phage genome. The putative protein product of vir contains a classic prokaryotic lipoprotein signal sequence and is a strong candidate for the MAV1-encoded virulence determinant.
RE.CNT 27
RE
(1) Barondess, J; J Bacteriol 1995, V177, P1247 HCAPLUS
(2) Bornberg-Bauer, E; Nucleic Acids Res 1998, V26, P2740 HCAPLUS
(3) Chuba, P; Mol Gen Genet 1989, V216, P287 HCAPLUS
(4) Cole, B; Immunol Today 1991, V12, P271 HCAPLUS
(6) Dybvig, K; Ann Rev Microbiol 1996, V50, P25 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> D BIB ABS L28 7

L28 ANSWER 7 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:374625 HCAPLUS
DN 129:145316
TI Real-time reporter of protein synthesis inhibition
AU Korpela, Matti; Virta, Marko; Karp, Matti
CS Department of Biotechnology, University of Turku, Finland
SO Methods Mol. Biol. (Totowa, N. J.) (1998), 102(Bioluminescence Methods and Protocols), 161-168
CODEN: MMBIED; ISSN: 1064-3745
PB Humana Press Inc.
DT Journal
LA English
AB This chapter presents a bioluminescent assay that describes a built-in amplification system for the screening and study of chem. substances with an inhibitory effect on protein synthesis. This real-time in vivo approach for protein synthesis inhibition using living bacteria fulfills a major need for the understanding of drug-receptor action. The method also works well with lyophilized bacteria, and the time needed for the assay is less than an hour. Thus, the assay is suitable for rapid and extremely sensitive screening of lead chems. (antimicrobial drug candidates) from combinatorial libraries. This assay is based on the measurement of real-time in vivo light prodn. of recombinant Escherichia coli bacteria expressing luciferase genes. In the described assay, vectors are used for efficient regulation of protein (luciferase) synthesis for studying drugs affecting protein synthesis. The very strong bacteriophage .lambda. leftward promoter (PL) is used which represses luciferase synthesis at suboptimal temps. (<36 degrees celcius). Protein synthesis can be efficiently switched on by brief heat shock (42 degrees celcius), which activates a mutant .lambda. repressor protein. The incubation of a drug with bacterial cells is performed prior to the induction of .lambda. PL-directed protein synthesis. After a heat shock, the luciferase synthesis is measured with a luminometer. The difference in the results when compared to noninhibited control samples reveals the influence of the drug candidate on protein synthesis in situ.

=> D BIB ABS L28 8

L28 ANSWER 8 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:192736 HCAPLUS
DN 128:202625
TI Identification of bacteriophage T4 virion proteins by transverse pore-gradient sodium dodecyl sulfate-polyacrylamide gel electrophoresis and dual amino acid labeling
AU Ferguson, Peter L.; Coombs, David H.
CS Div. Molecular Microbiology, Dep. Biology, Univ. New Brunswick, Fredericton, NB, E3B 6E1, Can.
SO Electrophoresis (1997), 18(15), 2880-2892
CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
AB A horizontal N,N'-methylenebisacrylamide (Bis) acryl-amide gradient sodium dodecyl sulfate (SDS) gel system was developed that permits the evaluation of the purity of individual protein bands in complex mixts. A Bis gradient gel is poured vertically and, after polymn., reoriented horizontally. A single large sample spanning the top of the gel is then run down at right angles to the gradient. The relative mobility of a few proteins varies considerably from the rest, causing them to merge with and cross other bands as the Bis concn. changes. Band splitting revealed that several bands previously thought to represent a single species are actually comprised of comigrating proteins. Once the Bis/monomer concn. offering the best sepn. was identified, we sought a simple method for identifying the genetic origin of bands, since many proteins now migrated in new positions on the gel. We reasoned that if infected cells were simultaneously labeled with [35S]methionine and [3H]leucine and the purified virion proteins analyzed to det. their 35S/3H ratio, we could identify most proteins by comparing this ratio with one calcd. from the T4 DNA sequence. Our expectations were realized, and we here report the sepn. and identification of all T4 virion proteins. Finally, we comment on the incorporation of various changes to the original Laemmli SDS-polyacrylamide gel formulations that have been reported in the literature.

=> D BIB ABS L28 9

L28 ANSWER 9 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:133302 HCAPLUS
DN 128:291641
TI A peptide inhibitor of cholesteryl ester transfer protein identified by screening a bacteriophage display library
AU Bonin, Paul D.; Bannow, Carol A.; Smith, Clark W.; Fischer, H. David; Erickson, Laurence A.
CS Cancer Research, Pharmacia and Upjohn, Kalamazoo, MI, USA
SO J. Pept. Res. (1998), 51(3), 216-225
CODEN: JPERFA; ISSN: 1397-002X
PB Munksgaard International Publishers Ltd.
DT Journal
LA English
AB We screened a bacteriophage display library of random decapeptides to identify peptide inhibitors of cholesteryl ester transfer protein (CETP). After affinity selection against CETP, bacteriophage-infected Escherichia coli were plated at clonal d. and 36 random clones were isolated. Anal. of the relevant portion of the bacteriophage DNA from a group of 12 clones that had a relatively high affinity for CETP revealed that the corresponding amino acid sequences of the displayed peptides exhibited an ... Xaa-Arg-Met-Arg-Tyr-Xaa ... composite motif. Based on those results, decapeptides from this group were synthesized and one of them, DP1 (NH2-VTWRMWYVPA-COOH), inhibited CETP-catalyzed transfer of cholesteryl esters and triglycerides. Amino- and carboxy-terminal truncations of DP1 demonstrated that the original decapeptide could be reduced to a pentapeptide without loss of either its ability to bind to CETP or its ability to inhibit CETP-mediated lipid transfer. That pentapeptide, NH2-WRMWY-COOH (WRMWY, PNU-107368E), binds directly to CETP and its inhibition is consistent with that of a competitive inhibitor of CETP with a Ki of 164 .mu.M. WRMWY or modified versions of this peptide may be useful in studying the interactions between CETP and plasma lipoproteins.

=> D BIB ABS L28 10

L28 ANSWER 10 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:710510 HCAPLUS
DN 128:31609
TI Molding a peptide into an RNA site by in vivo peptide evolution
AU Harada, Kazuo; Martin, Shelley S.; Tan, Ruoying; Frankel, Alan D.
CS Department of Biochemistry and Biophysics, University of California, San Francisco, CA, 94143-0448, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1997), 94(22), 11887-11892
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Short peptides corresponding to the arginine-rich domains of several RNA-binding proteins are able to bind to their specific RNA sites with high affinities and specificities. In the case of the HIV-1 Rev-Rev response element (RRE) complex, the peptide forms a single .alpha.-helix that binds deeply in a widened, distorted RNA major groove and makes a substantial set of base-specific and backbone contacts. Using a reporter system based on antitermination by the bacteriophage .lambda. N protein, it has been possible to identify novel arginine-rich peptides from combinatorial libraries that recognize the RRE with affinities and specificities similar to Rev but that appear to bind in nonhelical conformations. Here we have used codon-based mutagenesis to evolve one of these peptides, RSG-1, into an even tighter binder. After two rounds of evolution, RSG-1.2 bound the RRE with 7-fold higher affinity and 15-fold higher specificity than the wild-type Rev peptide, and in vitro competition expts. show that RSG-1.2 completely displaces the intact Rev protein from the RRE at low peptide concns. By fusing RRE-binding peptides to the activation domain of HIV-1 Tat, we show that the peptides can deliver Tat to the RRE site and activate transcription in mammalian cells, and more importantly, that the fusion proteins can inhibit the activity of Rev in chloramphenicol acetyltransferase reporter assays. The evolved peptides contain proline and glutamic acid mutations near the middle of their sequences and, despite the presence of a proline, show partial .alpha.-helix formation in the absence of RNA. These directed evolution expts. illustrate how readily complex peptide structures can be evolved within the context of an RNA framework, perhaps reflecting how early protein structures evolved in an "RNA world.".

=> D BIB ABS L28 11

L28 ANSWER 11 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:679261 HCAPLUS
DN 127:341781
TI Identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery
IN Pirozzi, Gregorio; Kay, Brian K.; Fowlkes, Dana M.
PA Cytogen Corp., USA; University of North Carolina,Chapel Hill
SO PCT Int. Appl., 220 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9737223	A1	19971009	WO 1997-US5547	19970403
	W: AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CU, CZ, EE, GE, GH, HU, IL, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	US 6011137	A	20000104	US 1996-630916	19960403
	CA 2250866	AA	19971009	CA 1997-2250866	19970403
	AU 9726597	A1	19971022	AU 1997-26597	19970403
	EP 897541	A1	19990224	EP 1997-918509	19970403
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2000508071	T2	20000627	JP 1997-535598	19970403
PRAI	US 1996-630916	19960403			
	WO 1997-US5547	19970403			

AB Novel polypeptides having WW domains of interest are described, along with DNA sequences that encode the same. A method of identifying these polypeptides by means of a sequence-independent (i.e., independent of the primary sequence of the polypeptide sought), recognition unit-based functional screen is also disclosed. Various applications of the method and of the polypeptides identified are described, including their use in assay kits for drug discovery, modification, and refinement.

=> D IND 11

L28 ANSWER 11 OF 35 HCAPLUS COPYRIGHT 2001 ACS
IC ICM G01N033-567
ICS G01N033-574; G01N033-48; A61K038-06; A61K038-16; C07K001-00; C07K005-00; C07K007-00; C07K014-00; C07K016-00; C07K017-00
CC 1-1 (Pharmacology)
Section cross-reference(s): 3, 9, 63
ST sequence protein WW domain drug discovery
IT Protein motifs
(HECT domain; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)
IT Protein motifs
(WW domain; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)
IT Genes (animal)
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(WWP1; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)
IT Genes (animal)
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(WWP2; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)
IT Genes (animal)
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(WWP3; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)
IT Genes (animal)

RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(WWP4; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Avidins
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(complexes; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Antigens
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(epitopes; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Biotinylation
Color formers
Cosmids
DNA sequences
Drug screening
Genetic vectors
Molecular cloning
Nucleic acid hybridization
Peptide library
Plasmids
Protein sequence analysis
Protein sequences
cDNA sequences
(identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Antibodies
Monoclonal antibodies
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Fusion proteins (chimeric proteins)
RL: ARU (Analytical role, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Promoter (genetic element)
RL: PEP (Physical, engineering or chemical process); PRP (Properties); PROC (Process)
(identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Proteins (general), biological studies
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Proteins (specific proteins and subclasses)
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(immobilized; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Bacteriophage
Virus
(proteins of; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT Drug delivery systems
(targeted; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT 192394-09-5P 198028-55-6P, Protein WWP1 (human gene WWP1)
198028-56-7P, Protein WWP2 (human gene WWP2) 198028-58-9P, Protein WWP4 (human gene WWP4)
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT 58-85-5, Biotin
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT 9001-78-9D, Alkaline phosphatase, streptavidin conjugates
RL: ARU (Analytical role, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(identification and isolation of novel polypeptides having WW domains for use in targetable drug discovery)

IT 197769-27-0 197769-28-1 197769-29-2 197769-30-5 197769-31-6
197769-32-7 197769-33-8 197769-34-9 197769-35-0 197769-36-1
197769-37-2 197769-38-3 197769-39-4 197769-40-7 197769-41-8
197769-42-9 197769-43-0 197769-44-1 197769-45-2 197769-46-3
197769-47-4 197769-48-5 197769-49-6 197769-50-9 197769-51-0
197769-52-1 197769-53-2 197769-54-3 197769-55-4 197769-56-5
197769-57-6 197769-58-7 197769-59-8 197769-60-1 197769-61-2
197769-62-3 197769-63-4 197769-64-5 197769-65-6 197769-66-7
197769-67-8 197769-68-9 197769-69-0 197769-70-3 197769-71-4
197769-72-5 197769-73-6 197769-74-7 197769-75-8 197769-76-9
197922-73-9 197922-74-0 197922-75-1 197922-76-2 197922-77-3
197922-80-8 197922-81-9 197922-83-1 197922-84-2
RL: BPR (Biological process); PRP (Properties); THU (Therapeutic use);
BIOL (Biological study); PROC (Process); USES (Uses)
(identification and isolation of novel polypeptides having WW domains
for use in targetable drug discovery)

IT 9013-20-1, Streptavidin
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES
(Uses)
(identification and isolation of novel polypeptides having WW domains
for use in targetable drug discovery)

IT 190047-92-8P 190047-94-0P 198028-57-8P, DNA (human gene WWP4
cDNA plus flanks) 198086-47-4P, DNA (human gene WWP2 cDNA plus
flanks)
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP
(Properties); BIOL (Biological study); OCCU (Occurrence); PREP
(Preparation)
(nucleotide sequence; identification and isolation of novel
polypeptides having WW domains for use in targetable drug discovery)

IT 73-22-3, Tryptophan, biological studies
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU
(Occurrence)
(protein WW domains contg.; identification and isolation of novel
polypeptides having WW domains for use in targetable drug discovery)

=> D BIB ABS L28 12

L28 ANSWER 12 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:372404 HCAPLUS
DN 127:134485
TI A region of vitamin K-dependent protein S that binds to C4b binding protein (C4BP) identified using bacteriophage peptide display libraries
AU Linse, Sara; Hardig, Ylva; Schultz, David A.; Dahlback, Bjorn
CS Dep. Physical Chem. 2, Lund Univ., Lund, S-221 00, Swed.
SO J. Biol. Chem. (1997), 272(23), 14658-14665
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Vitamin K-dependent protein S, a blood coagulation inhibitor, interacts with the C4b-binding protein (C4BP) in human plasma with high affinity (KD = 0.1 nM). Identification of a portion of protein S that binds to C4BP has been approached using random libraries of 6- and 15-mer peptides displayed on bacteriophage surfaces. Bacteriophage binding to the .beta.-chain of C4BP were selected in several rounds of affinity purifn. with intervening amplification in E. coli. Homol. searches of the affinity purified peptide sequences against protein S led to the identification of four regions in protein S that were similar to several of the selected peptides. These regions were synthesized as linear peptides and tested in inhibition expts. Only one distinct peak (around position 450) was obsd. when the homol. scores vs. human protein S sequence were averaged over all affinity purified peptides. A synthetic peptide comprising residues 439-460 in human protein S was found to inhibit protein S binding to C4BP. The same result was found with two overlapping peptides (residues 447-468 and 435-468, resp.) in a second set of synthetic peptides. Direct binding of the peptides to C4BP was inferred from titrns. monitored by recording the near UV CD spectra or the polarization of tryptophan fluorescence. The results suggest that residues 447-460 constitute a portion of protein S that is important for the interaction with C4BP. These findings may have implications for patients suffering from thrombosis, due to the lack of free protein S, by directing the design of drugs that disrupt protein S binding to C4BP.

=> D BIB ABS L28 13

L28 ANSWER 13 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:208424 HCAPLUS
DN 126:302789
TI Module swaps between related translocator proteins pIVf1, pIVIKe and PulD: identification of a specificity domain
AU Daefler, Simon; Russel, Marjorie; Model, Peter
CS Rockefeller University, New York, NY, 10021, USA
SO J. Mol. Biol. (1997), 266(5), 978-992
CODEN: JMOBAK; ISSN: 0022-2836
PB Academic
DT Journal
LA English
AB In Gram-neg. bacteria, type II and type III secretion and filamentous phage assembly systems use related outer membrane proteins for substrate-specific transport across the outer membrane. We show here that the specificity domain of the phage f1 outer membrane protein pIV is contained within the 149 N-terminal amino acid residues. When the pIVf1 specificity domain is fused to the translocator domain of the related pIV of phage IKe, the chimeric construct supports f1 but not IKe assembly. Functional coupling between the two domains in this chimeric construct is poor and is improved by a single amino acid change in the translocator domain of the pIVIKe. In native pIVIKe, two amino acid changes within its specificity domain are both necessary and sufficient to change the specificity from IKe to f1 assembly. Anal. of 39 chimeric constructs between pIVf1 and the outer membrane protein PulD of the pullulanase secretion system failed to identify a comparable exchangeable specificity domain. These results indicate that the two domains may not function autonomously, and suggest that tertiary and quaternary changes of the entire translocator component rather than of an autonomous functional domain are required for specific translocation across the outer membrane.

=> D BIB ABS L28 14

L28 ANSWER 14 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:73780 HCAPLUS
DN 126:196029
TI Identification of the bacteriophage T5 dUTPase by protein sequence comparisons
AU Kaliman, Alexander V.
CS Inst. Biochem. and Physiology Microorganisms, Russian Acad. Sci., Moscow, 142292, Russia
SO DNA Sequence (1996), 6(6), 347-350
CODEN: DNSEES; ISSN: 1042-5179
PB Harwood
DT Journal
LA English
AB It is shown by protein sequence comparisons that a 148 amino acid open reading frame (ORF 148) located at 67% of the bacteriophage T5 genome encodes a protein with strong similarity to known dUTPases. This protein contains five characteristic amino acid sequence motifs that are common to the dUTPase gene family. A similarity in size and high degree of sequence identity strongly suggest that the protein encoded by the ORF 148 of bacteriophage T5 is dUTPase.

=> D BIB ABS L28 15

L28 ANSWER 15 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:536117 HCAPLUS
DN 125:188768
TI Capsid targeting sequence targets foreign proteins into bacteriophage T4 and permits proteolytic processing
AU Mullaney, Julienne M.; Black, Lindsay W.
CS Sch. Med., Univ. Maryland, Baltimore, MD, 21201-1596, USA
SO J. Mol. Biol. (1996), 261(3), 372-385
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB A membrane-independent morphogenetic viral signal peptide is identified with bacteriophage T4 internal protein III (IPIII). Utilizing a phage-derived expression-packaging-processing system, which packages foreign proteins fused with IPIII into the phage capsid, a synthetic cleavage site introduced at the C-terminus of IPIII is demonstrated to be functional and permits processing of fusion proteins. IPIII, which possesses a native P21 cleavage site at its N terminus, is altered to possess a second P21 cleavage site at its C terminus where cleavage occurs by means of the scaffold proteinase P21 within the capsid. The altered IPII was inserted into an expression vector to permit on the creation of fusion proteins with staphylococcal nuclease, EcoRI endonuclease, .beta.-globin, and luciferase. Western immunoblot anal. of packaged T4eG326 indicates that the IPII:fusion-proteins are packaged into phage and proteolytically processed, thus the synthetic P21 cleavage site positioned at the C terminus are packaged per capsid. Truncation expts. identified the min. portion of IPIII required to achieve targeting into the phage capsid as a ten amino acid residue from the N terminus, which includes the N-terminal methionine residue and the proteinase P21 cleavage site, designated the CTS (capsid targeting sequence). The addn. of the CTS to a fragment of luciferase permits the protein to be packaged and processed, which demonstrates that the CTS is by itself sufficient to target foreign protein to the capsid. The imputed dual function of the CTS is supported by site-directed PCR mutagenesis, which reveals two functionally sep. domains of the CTS is by itself sufficient to target foreign protein to the capsid. The imputed dual function of the CTS is supported by site-directed PCR mutagenesis, which reveals two functionally sep. domains of the CTS for targeting and processing. The CTS appears to function in a core-related targeting mechanism that directs a polymorphic set of proteins into the T-even capsid or scaffold. Although structure formation is often assumed to involve extended protein interfaces, the anal. shows that a limited but specific sequence, the CTS, drives the interaction required to achieve targeting.

=> D IND 15

L28 ANSWER 15 OF 35 HCAPLUS COPYRIGHT 2001 ACS
CC 6-3 (General Biochemistry)
Section cross-reference(s): 10
ST capsid targeting sequence T4 packaging proteolysis
IT Proteins, biological studies
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(capsid targeting sequence targets foreign proteins into bacteriophage T4 and permits proteolytic processing)
IT Virus, bacterial
(T4, capsid targeting sequence targets foreign proteins into bacteriophage T4 and permits proteolytic processing)
IT Virion structure
(capsid, capsid targeting sequence targets foreign proteins into bacteriophage T4 and permits proteolytic processing)

=> D BIB ABS L28 16

L28 ANSWER 16 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:14924 HCAPLUS
DN 124:78292
TI A protein linkage map of Escherichia coli bacteriophage T7
AU Bartel, Paul L.; Roecklein, Jennifer A.; SenGupta, Dhruba; Fields, Stanley
CS Department Molecular Genetics and Microbiology, State University New York, Stony Brook, NY, 11794, USA
SO Nat. Genet. (1996), 12(1), 72-7
CODEN: NGENEC; ISSN: 1061-4036
DT Journal
LA English
AB Genome sequencing projects are predicting large nos. of novel proteins, whose interactions with other proteins must mediate the function of cellular processes. To analyze these networks, we used the yeast two-hybrid system on a genome-wide scale to identify 25 interactions among the proteins of Escherichia coli bacteriophage T7. Among these is a set of six interactions connecting proteins that function in DNa replication and DNA packaging. Remarkably, two genes, arranged such that one entirely overlaps the other and uses a different reading frame, encode interacting proteins. Several of the interactions reflect intramol. assocns. of different domains of the same polypeptide, suggesting that the two-hybrid assay may be useful in the anal. of protein folding. This global approach to protein-protein interactions may be applicable to the anal. of more complex genomes whose sequences are becoming available.

=> D BIB ABS L28 17

L28 ANSWER 17 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1995:974543 HCAPLUS
DN 124:78032
TI Sequencing and analysis of the prolate-headed lactococcal bacteriophage c2 genome and identification of the structural genes
AU Lubbers, Mark W.; Waterfield, Nick R.; Beresford, Tom P. J.; Le Page, Richard W. F.; Jarvis, Audrey W.
CS Biological Science Section, New Zealand Dairy Research Institute, Palmerston North, CB2 1QP, N. Z.
SO Appl. Environ. Microbiol. (1995), 61(12), 4348-56
CODEN: AEMIDF; ISSN: 0099-2240
DT Journal
LA English
AB The 22,163-bp genome of the lactococcal prolate-headed phage c2 was sequenced. Thirty-nine open reading frames (ORFs), early and late promoters, and a putative transcription terminator were identified. Twenty-two ORFs were in the early gene region, and 17 were in the late gene region. Putative genes for a DNA polymerase, a recombination protein, a sigma factor protein, a transcription regulatory protein, holin proteins, and a terminase were identified. Transcription of the early and late genes proceeded divergently from a noncoding 611-bp region. A 521-bp fragment contained within the 611-bp intergenic region could act as an origin of replication in Lactococcus lactis. Three major structural proteins, with sizes of 175, 90, and 29 kDa, and eight minor proteins, with sizes of 143, 82, 66, 60 44, 42, 32, and 28 kDa, were identified. Several of these proteins appeared to be posttranslationally modified by proteolytic cleavage. The 175- and 90-kDa proteins were identified as the major phage head proteins, and the 29- and 60-kDa proteins were identified as the major tail protein and (possibly) the tail adsorption protein, resp. The head proteins appeared to be covalently linked multimers of the same 30-kDa gene product. Phage c2 and prolate-headed lactococcal phage bIL67 (C. Schouler, S. D. Ehrlich, and M.-C. Chopin, Microbiol. 140:3061-3069, 1994) shared 80% nucleotide sequence identity. However, several DNA deletions or insertions which corresponded to the loss or acquisition of specific ORFs, resp., were noted. The identification of direct nucleotide repeats flanking these sequences indicated that recombination may be important in the evolution of these phages. Several poorly conserved ORFs and a poorly conserved module contg. several structural genes that might be involved in phage-specific properties, such as host range detn., were identified.

=> D BIB ABS L28 18

L28 ANSWER 18 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1995:814685 HCAPLUS
DN 123:331618
TI Identification of a gene encoding a bacteriophage-related integrase in a vap region of the Dichelobacter nodosus genome
AU Cheetham, Brian F.; Tattersall, David B.; Bloomfield, Garry A.; Rood, Julian I.; Katz, Margaret E.
CS Department of Biochemistry, Microbiology and Nutrition, University of New England, Armidale, N.S.W., 2351, Australia
SO Gene (1995), 162(1), 53-8
CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB Dichelobacter nodosus is the principal causative agent of ovine footrot. Nucleotide (nt) sequences from the D. nodosus genome have been isolated and a series of overlapping .lambda. clones defining vap (virulence-assocd. protein) regions 1, 2 and 3 have been reported [Katz et al., J. Bacteriol. 176 (1994) 2663-2669]. In the present study, the limits of the virulence-assocd. (va) DNA around vap regions 1 and 3 were detd. by dot-blot hybridization expts. using plasmid subclones to probe genomic DNA from the D. nodosus virulent strain A198 and the benign strain C305. This va region was found to be approx. 11.9kb in length, and to be interrupted by a short DNA segment which is also found in the benign D. nodosus strain. Sequence anal. of the entire region revealed an ORF, intA, which is very similar to the integrases of bacteriophages .phi.R73, P4 and Sf6. Bacteriophages .phi.R73 and P4 integrate into the 3' ends of tRNA genes, with the integrase genes adjacent to the tRNA genes. A similar arrangement was found in the D. nodosus va region. A 19-bp nt sequence was found to be repeated at the ends of the va region, and may represent the bacteriophage attachment site. These findings suggest that D. nodosus may have acquired these DNA sequences by the integration of a bacteriophage, or an integrative plasmid that contains a bacteriophage-related integrase gene. The high similarity of the D. nodosus integrase to integrases from coliphages suggests that these va sequences may be transferred between distantly related bacteria. Integration of the putative bacteriophage was followed by at least two independent duplication events.

=> D BIB ABS L28 19

L28 ANSWER 19 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1995:796092 HCAPLUS
DN 123:331531
TI Characterization of a new rho mutation that relieves polarity of Mu insertions
AU Peters, Joseph E.; Benson, Spencer A.
CS Dep. Microbiology, Univ. Maryland, College Park, MD, 20742, USA
SO Mol. Microbiol. (1995), 17(2), 231-40
CODEN: MOMIEE; ISSN: 0950-382X
DT Journal
LA English
AB The authors report the identification and characterization of a new rho mutation, rho614, that relieves polarity of Mu insertions in Escherichia coli. The mutation was identified by its ability to suppress the polarity of the Mu-mediated .PHI.(lamB'-'lacZ)hyb61-4 fusion that is located at codon four of the lamB signal sequence. The rho614 mutation alters residue 80 in the proposed RNA-binding domain of Rho and is recessive to wild-type rho. The authors suggest that in the presence of the rho614 allele transcripts initiated at the Mu promoter PcM fail to terminate at presumptive Rho-dependent termination sites, namely rut1 and rut2, and continue into the 3' lamB gene allowing a LamB+ phenotype. This contention is supported by deletion anal. of the region and the observation that insertional inactivation of genes that reduce transcription from PcM, clpP (ATP protease), himA (IHF-.alpha.), and himD (IHF-.beta.), block the LamB+ phenotype. Rho614, rho4 and rho201 alleles suppress the polarity of a malK::Mu insertion on the downstream lamB gene. However, the polarity of the .PHI.(lamB'-'lacZ)hyb61-4 insertion is only suppressed by the rho614 mutation. The authors propose that the rho614 mutation allows suppression of transcriptional polarity without interfering with translation initiation signals of the truncated 'lamB gene. In addn. to identifying a new rho mutation and Rho-dependent terminator sequence, this system provides a means of studying Rho protein/terminator relationships through the identification of new classes of rho mutations.

=> D BIB ABS L28 20

L28 ANSWER 20 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1994:317101 HCAPLUS
DN 120:317101
TI Analysis of cis and trans acting elements required for the initiation of DNA replication in the Bacillus subtilis bacteriophage SPP1
AU Pedre, Xiomara; Weise, Frank; Chai, Sunghee; Lueder, Gerhild; Alonso, Juan C.
CS Max-Planck-Inst. Mol. Genet., Berlin, D-14195, Germany
SO J. Mol. Biol. (1994), 236(5), 1324-40
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB The development of SPP1 has been studied in several B. subtilis mutants conditionally defective in initiation of DNA replication. Initiation of SPP1 replication is independent of the host DnaA (replisome organizer), DnaB, DnaC and DnaI products, but requires the DnaG (DNA primase) and the DNA gyrase. Furthermore, SPP1 replication is independent of the DnaK (heat shock) protein. The phage-encoded products required for initiation of SPP1 replication have been genetically characterized. Anal. of the nucleotide sequence (3.292 kilobases) of the region where SPP1 initiation replication mutants map, revealed five open reading frames (orf). The authors have assigned genes 38, 39 and 40 to three of these orfs, which have the successive order gene 38-gene 39-orf39.1-gene 40-orf41. The direction of transcription of the reading frames, the lengths of the mRNAs as well as the transcription start point, upstream of gene 38 (PE2), were identified. Proteins of 29.9, 14.6 and 46.6 kDa were anticipated from translation of gene 38, gene 39 and gene 40, resp. The purified G38P and G39P have estd. mol. masses of 31 and 15 kDa. G38P and G39P do not share significant identity with primary protein sequences currently available in protein databases, whereas G40P shares substantial homol. with a family of DNA primase-assocd. DNA helicases. G38P binds specifically to two discrete SPP1 DNA restriction fragments (EcoRI-4 and EcoRI-3). The G38P binding site on EcoRI-4 was localized on a 393 bp DNA segment, which lies within the coding sequence of gene 38. The putative binding site on EcoRI-3 was inferred by DNA sequence homol., it maps in a non-coding segment. G39P, which does not bind to DNA, is able to form a complex with G38P. The organization of the SPP1 genes in the gene 38 to gene 40 interval resembles that one found in the replication origin regions of different Escherichia coli double-standed DNA phages (.lambda., .phi.80 and P22). The authors propose that the conserved gene organization is representative of the replication origin region of a primordial phage.

=> D BIB ABS L28 21

L28 ANSWER 21 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1994:212209 HCAPLUS
DN 120:212209
TI Identification of bacteriophage T4 prereplicative proteins on two-dimensional polyacrylamide gels
AU Kutter, Elizabeth M.; d'Acci, Kathy; Drivdahl, Rolf H.; Gleckler, Jan; McKinney, John C.; Peterson, Shane; Guttman, Burton S.
CS Evergreen State Coll., Olympia, WA, 98505, USA
SO J. Bacteriol. (1994), 176(6), 1647-54
CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Bacteriophage T4 makes a large no. of prereplicative proteins, which are involved in directing the transition from host to phase functions, in producing the new T4 DNA, and in regulating transcriptional shifts. The authors have used two-dimensional gel electrophoresis (nonequil. pH gradient electrophoresis gels in the first dimension and sodium dodecyl sulfate-polyacrylamide gradient slab gels in the second) to identify a no. of new prereplicative proteins. The products of many known genes are identified because they are missing in mutants with amber mutations of those genes, as analyzed by the authors and/or previous workers. Some have also been identified by running purified proteins as markers on gels with labeled exts. from infected cells. Other proteins that are otherwise unknown are characterized as missing in infections with phage carrying certain large deletions and, in some cases, are collected with sequence data.

=> D IND 21

L28 ANSWER 21 OF 35 HCAPLUS COPYRIGHT 2001 ACS
CC 10-1 (Microbial, Algal, and Fungal Biochemistry)
ST bacteriophage T4 prereplicative protein gel electrophoresis
IT Proteins, biological studies
RL: BIOL (Biological study)
(prereplicative, of bacteriophage T4, gel electrophoresis of)
IT Virus, bacterial
(T4, prereplicative proteins of, gel electrophoresis identification of)

=> D BIB ABS L28 22

L28 ANSWER 22 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:576365 HCAPLUS
DN 119:176365
TI Isolation and characterization of ClpX, a new ATP-dependent specificity component of the Clp protease of Escherichia coli
AU Wojtkowiak, Diana; Georgopoulos, Costa; Zylicz, Maciej
CS Dep. Mol. Biol., Univ. Gdansk, Pol.
SO J. Biol. Chem. (1993), 268(30), 22609-17
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The authors have used 14C-labeled **bacteriophage** .lambda.O-DNA replication **protein** as a probe to **identify** and purify Escherichia coli proteases capable of its degrdn. In this manner, five different proteases (termed Lop) have been identified capable of degrading .lambda.O protein to acid-sol. fragments in an ATP-dependent fashion. One of these activities was purified to homogeneity and shown to be composed of two different polypeptides. The 23,000-Da component (LopP) was identified as the previously characterized ClpP protein, known to complex with ClpA to form the ClpAP, an ATP-dependent protease, capable of degrading casein. The second 46,000-Da component was identified as ClpX (LopC), coded by a **gene** located in the same operon, but promoter distal to that coding for ClpP (see accompanying paper). This identification was based on the detn. of the **sequence** of the first 24 amino acid residues of the purified ClpX protein and its identity with that predicted by the DNA **sequence**. The ClpXP protease is substrate specific, degrades casein (known to be degraded by ClpAP), .lambda.P, or DnaK proteins slowly or not at all. These results suggest that ClpX protein directs ClpP protease to specific substrates. It is estd. that 50% of all .lambda.O-specific protease activity present in crude E. coli exts. is due to the ClpXP protease. The authors propose that transient inhibition of .lambda.O degrdn. obsd. in vivo during the later stages of .lambda.-DNA replication in vivo is responsible for the switch from bidirectional to unidirectional replication. One round unidirectional replication will lead to strand sepn. resulting in a switch from early (theta) to late (sigma) mode of .lambda.-DNA replication.

=> D BIB ABS L28 23

L28 ANSWER 23 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:510527 HCAPLUS
DN 119:110527
TI The linear mitochondrial plasmid pAL2-1 of a long-lived Podospora anserina mutant is an invertron encoding a DNA and RNA polymerase
AU Hermanns, Josef; Osiewacz, Heinz D.
CS Forschungsschwerpunkt: Angew. Tumorvirol., Dtsch. Krebsforschungszent., Heidelberg, W-6900, Germany
SO Curr. Genet. (1992), 22(6), 491-500
CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB The mol. characterization of an addnl. DNA species (pAL2-1) which was identified previously in a long-lived extrachromosomal mutant (AL2) of Podospora anserina revealed that this element is a mitochondrial linear plasmid. PAL2-1 is absent from the corresponding wild-type strain, has a size of 8395 bp and contains perfect long terminal inverted repeats (TIRs) of 975 bp. Exonuclease digestion expts. indicated that proteins are covalently bound at the 5' termini of the plasmid. Two long, non-overlapping open reading frames, PRF1 (3,594 bp) and ORF2 (2847 bp), have been identified, which are located on opposite strands and potentially encode a DNA and RNA polymerase, resp. The ORF1-encoded polypeptide contains three conserved regions which may be responsible for a 3'-5' exonuclease activity and the typical consensus sequences for DNA polymerases of the D type. In addn., an amino-acid sequence motif (YSRLRT), recently shown to be conserved in terminal proteins from various bacteriophages, has been identified in P. anserina shares all characteristics with invertrons, a group of linear mobile genetic elements.

=> D BIB ABS L28 24

L28 ANSWER 24 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:489203 HCAPLUS
DN 119:89203
TI Identification of amino acid residues at the interface of a bacteriophage T4 regA protein-nucleic acid complex
AU Webster, Kevin R.; Keill, Sarah; Konigsberg, William; Williams, Kenneth R.; Spicer, Eleanor K.
CS Sch. Med., Yale Univ., New Haven, CT, 06511, USA
SO J. Biol. Chem. (1992), 267(36), 26097-103
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The bacteriophage T4 regA protein (Mr = 14,600) is a translational repressor of a group of T4 early mRNAs. To identify a domain of regA protein that is involved in nucleic acid binding, UV light was used to photochem. cross-link regA protein to [32P]p(dT)16. The cross-linked complex was subsequently digested with trypsin, and peptides were purified using anion exchange high performance liq. chromatog. Two tryptic peptides cross-linked to [32P]p(dT)16 were isolated. Gas-phase sequencing of the major cross-linked peptide yielded the following sequence: VISXKQKHEWK, which corresponds to residues 103-113 of regA protein. Phenylalanine 106 was identified as the site of crosslinking, thus placing this residue at the interface of the regA protein-p(dT)16 complex. The minor cross-linked peptide corresponded to residues 31-41, and the site of crosslinking in the peptide was tentatively assigned to Cys-36. The nucleic acid binding domain of regA protein was further examd. by chem. cleavage of regA protein into six peptides using CNBr. Peptide CN6, which extends from residue 95 to 122, retains both the ability to be cross-linked to [32P]p(dT)16 and 70% of the nonspecific binding energy of the intact protein. However, peptide CN6 does not exhibit the binding specificity of the intact protein. Three of the other individual CNBr peptides have no measurable affinity for nucleic acid, as assayed by photo-crosslinking or gel mobility shifts.

=> D BIB ABS L28 25

L28 ANSWER 25 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:250071 HCAPLUS
DN 118:250071
TI Structural relationship of bacterial RecA proteins to recombination proteins from bacteriophage T4 and yeast
AU Story, Randall M.; Bishop, Douglas K.; Kleckner, Nancy; Steitz, Thomas A.
CS Dep. Mol. Biophys., Yale Univ., New Haven, CT, 06511, USA
SO Science (Washington, D. C., 1883-) (1993), 259(5103), 1892-6
CODEN: SCIEAS; ISSN: 0036-8075
DT Journal
LA English
AB RecA protein is essential in eubacteria for homologous recombination and promotes the homologous pairing and strand exchange of DNA mols. in vitro. Recombination proteins with weak sequence similarity to bacterial RecA proteins have been identified in bacteriophage T4, yeast, and other higher organisms. Anal. of the primary sequence relationships of DMC1 from Saccharomyces cerevisiae and UvsX of T4 relative to the three-dimensional structure of RecA from Escherichia coli suggests that both proteins are structural homologs of bacterial RecA proteins. This anal. argues that proteins in this group are members of a single family that diverged from a common ancestor that existed prior to the divergence of prokaryotes and eukaryotes.

=> D BIB ABS L28 26

L28 ANSWER 26 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:248791 HCAPLUS
DN 118:248791
TI Identification of a family of bacteriophage T4 genes encoding protein similar to those present in group I introns of fungi and phage
AU Sharma, Mridula; Ellis, Richard L.; Hinton, Deborah M.
CS Lab. Biochem. Pharmacol., Natl. Inst. Diabetes Digest. Kidney Dis., Bethesda, MD, 20892, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1992), 89(14), 6658-62
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The bacteriophage T4 segA gene lies in a genetically unmapped region between the gene .beta.gt (.beta.-glucosyltransferase) and uvsX (recombination protein) and encodes a protein of 221 amino acids. The authors have found that the first 100 amino acids of the SegA protein are highly similar to the N termini of four other predicted T4 proteins, also of unknown function. Together these five proteins, SegA-E (similar to endonucleases of group I introns), contain regions of similarity to the endonuclease I-Tev I, which is encoded by the mobile group I intron of the T4 td gene, and to putative endonucleases of group I introns present in the mitochondria of Neurospora crassa, Podospora anserina, and Saccharomyces douglasii. Intron-encoded endonucleases are required for the movement (homing) of the intron DNA into an intronless gene, cutting at or near the site of intron insertion. In vitro assays indicate that SegA, like I-Tev I, is a Mg2+-dependent DNA endonuclease that has preferred sites for cutting. Unlike the I-Tev I gene, however, there is no evidence that segA (or the other seg genes) reside within introns. Thus, it is possible that segA encodes an endonuclease that is involved in the movement of the endonuclease-encoding DNA rather than in the homing of an intron.

=> D BIB ABS L28 27

L28 ANSWER 27 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:186811 HCAPLUS
DN 118:186811
TI The superfamily of UvrA-related ATPases includes three more subunits of putative ATP-dependent nucleases
AU Koonin, Eugene V.; Gorbalenya, Alexander E.
CS Inst. Microbiol., Moscow, 117811, Russia
SO Protein Sequences Data Anal. (1992), 5(1), 43-5
CODEN: PSDAE6; ISSN: 0931-9506
DT Journal
LA English
AB It is demonstrated that the amino acid sequences of the products of Escherichia coli genes sbcC and prrC, and bacteriophage P2 gene old encompass the four conserved motifs typical of the superfamily of UvrA-related ATPases. A more pronounced statistically significant similarity was revealed between SbcC protein, bacteriophage T4 endonuclease component gp46 and bacteriophage T5 protein D13. It is suggested that the newly identified members of the superfamily might all be ATPase components of the resp. nucleases, and that the reactions catalyzed by these enzymes are probably ATP dependent.

=> D BIB ABS L28 28

L28 ANSWER 28 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1991:600243 HCAPLUS
DN 115:200243
TI Expression of chimeric ras protein with OmpF signal peptide in Escherichia coli: localization of OmpF fusion protein in the inner membrane
AU Yamamoto, Takeshi; Okawa, Noriyuki; Endo, Tohru; Kaji, Akira
CS Res. Inst. Mol. Genet., Tsumura and Co., Ami, 300-11, Japan
SO Appl. Microbiol. Biotechnol. (1991), 35(5), 615-21
CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
AB The ras gene was fused with the DNA sequence of OmpF signal peptide or with the DNA sequence of OmpF signal peptide plus the amino terminal portion of the OmpF gene. They were placed in plasmids together with the bacteriophage .lambda. PL promoter. These plasmids were introduced into E. coli strain K-12 and the OmpF signal peptide fusion proteins were expressed. These fusion proteins were identified as 29.0 and 30.0 kDa proteins. However, processed products of these proteins were not found in the ext. The fusion proteins were localized mostly in the cytoplasm and the inner membrane, but none of them were secreted into the periplasmic space. On the other hand, the ras protein alone was found in the cytoplasm and not in the inner membrane. Viable counts of E. coli harbouring these plasmids decreased when these fused proteins were induced. Induction of the ras protein alone did not harm cells. These observations suggest that insertion of the heterologous proteins into the inner membrane may cause the bactericidal effect.

=> D IND 28

L28 ANSWER 28 OF 35 HCAPLUS COPYRIGHT 2001 ACS
CC 3-4 (Biochemical Genetics)
Section cross-reference(s): 6
ST Escherichia OmpF gene ras fusion protein
IT Proteins, specific or class
RL: BIOL (Biological study)
(OmpF, ras protein fusion with, of Escherichia coli, expression and membrane localization of)
IT Escherichia coli
(OmpF-ras fusion protein expression in, inner membrane localization of)
IT Protein sequences
(of OmpF-ras fusion protein, of Escherichia coli and Harvey murine sarcoma virus)
IT Virus, animal
(Harvey murine sarcoma, ras protein of, Escherichia coli OmpF protein fusion with, cellular localization and antibacterial activity of)
IT Microbicidal and microbiostatic action
(bactericidal, of OmpF-ras fusion protein, in Escherichia coli)
IT Lipoproteins
RL: BIOL (Biological study)
(gene ras, OmpF fusion with, of Harvey murine sarcoma virus, Escherichia coli expression of)
IT Deoxyribonucleic acid sequences
(protein F-specifying, of OmpF-ras, of Escherichia coli and Harvey murine sarcoma virus)

=> D BIB ABS L28 29

L28 ANSWER 29 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1989:626091 HCAPLUS
DN 111:226091
TI Sequence analysis and expression in Escherichia coli of the hyaluronidase gene of Streptococcus pyogenes bacteriophage H4489A
AU Hynes, Wayne L.; Ferretti, Joseph J.
CS Health Sci. Cent., Univ. Oklahoma, Oklahoma City, OK, 73190, USA
SO Infect. Immun. (1989), 57(2), 533-9
CODEN: INFIBR; ISSN: 0019-9567
DT Journal
LA English
AB The hyaluronidase gene (hylP) from S. pyogenes bacteriophage H4489A was previously cloned into E. coli plasmid pUC8 as a 3.1-kilobase ThaI fragment. Southern hybridization expts. confirmed the origin of this fragment in phage H4489A and the nucleotide sequence of the entire fragment was detd. Two open reading frames (ORFs) were found, the first of which specified a 39,515-mol.-wt. protein identified as the bacteriophage hyaluronidase. The second ORF encoded a 65,159-mol.-wt. protein of unknown function. Putative transcription and translation control sequences for each ORF were identified by using a plasmid contg. a promoterless chloramphenicol acetyltransferase gene. Controlled exclusive expression of the hylP gene via the T7 polymerase-promoter system in E. coli resulted in a 40,000-dalton protein, a result consistent with the coding capacity of the hylP gene.

=> D BIB ABS L28 30

L28 ANSWER 30 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1982:175150 HCAPLUS
DN 96:175150
TI Identification and mapping of five new genes in bacteriophage T7
AU Studier, F. William
CS Biol. Dep., Brookhaven Natl. Lab., Upton, NY, 11973, USA
SO J. Mol. Biol. (1981), 153(3), 493-502
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB 3-Factor crosses were used to describe and map mutations affecting the single-stranded DNA-binding protein of bacteriophage T7 (gene 2.5) and 4 T7 proteins of unknown function (the gene 4.3, 4.5, 4.7, and 5.5 proteins). The gene 2.5 mutation produced a slightly short DNA-binding protein; the corresponding nucleotide sequence contained only 1-3 readily mutable sites. The gene 4.3, 4.5, and 4.7 proteins (Mr .apprx.8000-15,000) were eliminated by a deletion mutant that removed most of the DNA between genes 4 and 5. The gene 5.5 protein (Mr .apprx.11,700) was made in relatively large amts. and was affected by 2 different mutations that were mapped between genes 5 and 6.

=> D BIB ABS L28 31

L28 ANSWER 31 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1982:158773 HCAPLUS
DN 96:158773
TI Solid-phase sequence analysis of polypeptides eluted from polyacrylamide gels. An aid to interpretation of DNA sequences exemplified by the Escherichia coli unc operon and bacteriophage lambda
AU Walker, John E.; Auffret, Anthony D.; Carne, Alan; Gurnett, Anne; Hanisch, Peter; Hill, Diana; Saraste, Matti
CS Lab. Mol. Biol., Med. Res. Counc. Cent., Cambridge, CB2 2QH, UK
SO Eur. J. Biochem. (1982), 123(2), 253-60
CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB An approach to sequencing proteins by the solid-phase method combined with isolation of proteins and polypeptides by gel electrophoresis is described. Mixts. of proteins or polypeptides resulting from digests are fractionated in the presence of dodecyl sulfate in polyacrylamide gels. They are detected with Coomassie Blue, eluted, selectively reacted with porous glass derivs. and sequenced in their N-terminal regions with the aid of a new microsequencer. Alternatively, they can be analyzed or digested with enzymes and fingerprinted. It is a relatively rapid method of purifying proteins for sequence anal. which was used to provide partial protein sequence data to complement DNA sequences. Nine genes, 4 from the unc operon E. coli encoding the .alpha., .beta., .gamma., and .epsilon. subunits of ATP synthase and 5 for capsid proteins of bacteriophage .lambda. were identified by this method. In addn., the method was used to study antigenic variation in trypanosomes and the enzyme 6-phosphogluconate dehydrogenase.

=> D OND 31

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IABS -------- ABS, indented with text labels
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SIBIB ------- IBIB, no citations

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HITIND ------ IC, ICA, ICI, NCL, CC and index field (ST and IT) containing hit terms

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HITSTR ------ HIT RN, its text modification, its CA index name, and
              its structure diagram
FHITSTR ----- First HIT RN, its text modification, its CA index name, and
              its structure diagram
KWIC -------- Hit term plus 20 words on either side
OCC --------- Number of occurrence of hit term and field in which it occurs
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=> D IND 31

L28 ANSWER 31 OF 35 HCAPLUS COPYRIGHT 2001 ACS
CC 9-10 (Biochemical Methods)
Section cross-reference(s): 3, 6
ST peptide sequencing gel electrophoresis; protein solid phase sequencing; DNA protein sequencing; Edman degrdn protein sequencing; Escherichia operon DNA protein sequencing; phage lambda DNA protein sequencing
IT Protein sequences
(detn. of, by gel electrophoresis and solid-phase Edman degrdn., DNA sequences in relation to)
IT Deoxyribonucleic acid sequences
(detn. of, protein sequences in relation to)
IT Gene and Genetic element
RL: ANST (Analytical study)
(for capsid proteins of bacteriophage .lambda. and F1 ATPase complex proteins of Escherichia coli, order of, protein sequences in relation to)
IT Escherichia coli
(genes for F1 ATPase complex proteins of, order of, protein sequences in relation to)
IT Trypanosoma brucei
(glycoprotein antigens of, sequencing of, DNA sequences in relation to)
IT Antigens
RL: ANST (Analytical study)
(glycoproteins, of Trypanosoma brucei, sequencing of, DNA sequences in relation to)
IT Proteins
RL: ANST (Analytical study)
(of capsid of bacteriophage .lambda. and of F1 ATPase complex of Escherichia coli, gene order for)
IT Edman degradation
(solid-phase, of proteins, gel electrophoresis in relation to)
IT Electrophoresis and Ionophoresis
(gel, of proteins, on polyacrylamide, for peptide sequencing, DNA sequences in relation to)
IT Virus, bacterial
(lambda, capsid proteins of, gene order for)
IT Operon
(unc, genes of, of Escherichia coli, order of, protein sequences in relation to)
IT 9000-83-3
RL: ANST (Analytical study)
(F1, gene for subunits of, of Escherichia coli, order of, protein sequences in relation to)
IT 9001-82-5
RL: ANST (Analytical study)
(sequencing of, DNA sequences in relation to)

=> D BIB ABS L28 32

L28 ANSWER 32 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1980:2910 HCAPLUS
DN 92:2910
TI **Identification of two new capsid proteins in bacteriophage M13**
AU Simons, Guus F. M.; Konings, Ruud N. H.; Schoenmakers, John G. G.
CS Lab. Mol. Biol., Univ. Nijmegen, Nijmegen, Neth.
SO FEBS Lett. (1979), 106(1), 8-12
CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB Electrophoretic anal. of the capsid proteins of phage M13 gave, in addn. to the 2 known coat proteins, 2 new proteins, designated as C and D, with mol. wts. of 3500 and 15,000, resp. The genes coding for these proteins were mapped by amino acid compn. studies and previously reported nucleotide sequences.

=> D IND 32

L28 ANSWER 32 OF 35 HCAPLUS COPYRIGHT 2001 ACS
CC 10-1 (Microbial Biochemistry)
ST protein capsid phage gene
IT Gene
RL: BIOL (Biological study)
(for capsid proteins of phage M13, mapping of)
IT Proteins
RL: BIOL (Biological study)
(of phage M13 capsid, compn. and gene mapping of)
IT Virus, bacterial
(M13, capsid proteins of, compn. and gene mapping for)

=> D BIB ABS L28 33

L28 ANSWER 33 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1979:2864 HCAPLUS
DN 90:2864
TI Identification of lysis protein E of bacteriophage .vphi.X174
AU Pollock, Thomas J.; Tessman, Ethel S.; Tessman, Irwin
CS Dep. Biol. Sci., Purdue Univ., West Lafayette, Indiana, USA
SO J. Virol. (1978), 28(1), 408-10
CODEN: JOVIAM; ISSN: 0022-538X
DT Journal
LA English
AB The product of gene E, the lysis gene of .vphi.X174, was identified as a distinct band in a Na dodecyl sulfate-electrophoresis gel. The position of the band was consistent with a mol. wt. of 10,589, calcd. from the nucleotide sequence of the gene. The band was eliminated by a nonsense mutation in gene E. It is estd. that .apprx.100-300 mols. of E protein are made in an infected cell; this appears to be <10% of the amt. of protein made by gene D, in which gene E is wholly contained.

=> D BIB ABS L28 34

L28 ANSWER 34 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1978:472803 HCAPLUS
DN 89:72803
TI **Identification of the N gene protein of bacteriophage .lambda.**
AU Shaw, Jocelyn E.; Jones, Barbara B.; Pearson, Mark L.
CS Dep. Med. Genet., Univ. Toronto, Toronto, Ont., Can.
SO Proc. Natl. Acad. Sci. U. S. A. (1978), 75(5), 2225-9
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The N gene protein, pN, of phage .lambda. stimulates early gene transcription by allowing mRNA chain elongation to proceed into genes distal to transcription termination sites normally recognized by the Escherichia coli transcription termination protein .rho.. The major form of pN in crude cell exts. of infected cells has an apparent mol. wt. of 13,500. A deletion-substitution mutant terminating in N, .lambda.bio256, codes for a shorter pN of mol. wt. 12,500. A nonsense fragment of 10,500 mol. wt. coded by .lambda.Nam7 has also been identified. It has also been possible to distinguish pN itself from other early .lambda. polypeptides by infecting ron- cells with either .lambda.Nmar phage allowing pN synthesis but not pN action or .lambda.Nam phage defective in pN synthesis and pN action. The possible existence of multiple mol. wt. forms of pN and the location of the coding sequences in the N gene region are discussed.

=> D BIB ABS L28 35

L28 ANSWER 35 OF 35 HCAPLUS COPYRIGHT 2001 ACS
AN 1978:116827 HCAPLUS
DN 88:116827
TI Detection of prokaryotic signal peptidase in an Escherichia coli membrane fraction: Endoproteolytic cleavage of nascent f1 pre-coat protein
AU Chang, Chung Nan; Blobel, Guenter; Model, Peter
CS Rockefeller Univ., New York, N. Y., USA
SO Proc. Natl. Acad. Sci. U. S. A. (1978), 75(1), 361-5
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB An inverted membrane vesicle fraction isolated from uninfected E. coli and largely derived from the inner membrane contained an endoproteolytic activity that cleaves nascent bacteriophage f1 pre-coat protein into 2 identifiable products. The electrophoretic mobility on Na dodecyl sulfate/urea/polyacrylamide gels and the partial N-terminal sequence of the larger fragment were indistinguishable from those of the mature phage coat protein. Partial N-terminal sequence anal. showed that the smaller fragment corresponds to the N-terminal signal peptide of f1 pre-coat protein. Cleavage occurred only if the membrane fraction was present during in vitro synthesis, and was not obsd. if it was added after completion of pre-coat protein synthesis. The cleavage reaction was strongly stimulated when the membrane fraction was present together with the nonionic detergent, Nikkol. These results are consistent with and discussed in terms of the signal hypothesis.

=> D BIB ABS L86

L86 ANSWER 1 OF 1 USPATFULL
AN 1999:146343 USPATFULL
TI Auxiliary gene and protein of methicillin resistant bacteria and antagonists thereof
IN Tomasz, Alexander, New York, NY, United States
De Lencastre, Herminia, New York, NY, United States
PA The Rockefeller University, New York, NY, United States (U.S. corporation)
PI US 5985643 19991116
AI US 1996-679635 19960710 (8)
DT Utility
EXNAM Primary Examiner: Carlson, Karen Cochrane
LREP Klauber & Jackson
CLMN Number of Claims: 5
ECL Exemplary Claim: 1
DRWN 12 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 2215
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is directed to the identification of mutant strains of methicillin resistant bacteria, in particular methicillin resistant Staphylococcus aureus, to identify the characteristics of such bacteria and develop drugs that can reverse, inhibit, or reduce bacterial resistance to beta lactam antibiotics, e.g., methicillin. The invention particularly relates to identification of a novel mutant strain of methicillin resistant S. aureus that manifests a unique phenotype, having a block in cell wall synthesis at or close to the branch point in hexose metabolism involved in the synthesis of cell wall components. Accordingly, the invention provides for methods of treatment and corresponding pharmaceutical compositions for treating bacterial, particularly staphylococcal, infections.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> D KWIC

L86 ANSWER 1 OF 1 USPATFULL
SUMM The present invention relates to the identification of auxiliary genes that encode proteins involved in antibiotic resistance in bacteria, and to compounds that can antagonize the activity of such proteins, thereby resensitizing resistant bacteria to antibiotics.
SUMM . . . world and the most "advanced" forms of these pathogens carry resistance mechanisms to all but one (vancomycin) of the usable antibacterial agents (Blumberg et al., 1991, J. Inf. Disease (63:1279-85).
SUMM . . . of vancomycin resistance to MRSA is only a matter of time. Once this happens, an invasive bacterial pathogen without any antibacterial agent to control it will result. This event would constitute nothing short of a potential public health disaster of immense. . . .
SUMM . . . in the parental bacterium to the low value of about 4 .mu.g/ml in the transposon mutant (Matthews and Tomasz, 1990, Antimicrobial Agents and Chemotherapy 34:1777-9).
SUMM . . . literature had risen to four; presently, six have been identified [Berger-Bachai, Trends in Microbiology, 2:389-392 (1994); DeLencastre et al., J. Antimicrob. Chemother. 33:7-24 (1994); Henze et al., J. Bacteriol. 175: 1612-1620 (1993); Maidhof et al., J. Bacteriol. 173:3507-3513 (1991)].
SUMM . . . were determined (as in the cases of the auxiliary genes known as femA, femB and femC) (Berger-Bachi et al., 1992, Antimicrobial Agents and Chemotherapy 36:1367-73; Gustafson et al., 1993, In Abstracts of the 93rd General Meeting of the American Society for. . . . Microbiology, Abstract A-97, p. 18; and De Lencastre et al., 1993, "Molecular Aspects of Methicillin resistance in Staphylococcus aureus", J. Antimicrob. Chemother. 33:), the genes were shown to have unique DNA sequences; and (iii) in the cases in which the mutants. . . .
SUMM . . . of methicillin resistance [International Patent Publication No. WO 95/16039, published Jun. 15, 1995 by DeLencastre and Tomasz; DeLencastre and Tomasz, Antimicrob. Agents. Chemother. 38:2590-2598 (1994)].
DRWD . . . The shuttle plasmid pGC2 was constructed by inserting the

plasmid pC194 into the PvuII site of pGEM-1 [Matthews and Tomasz, Antimicrob. Agents Chemother., 34:1777-79 (1990)]. The 2.2 kb insert fragment of pSW-4A was subcloned into EcoRi/Psl sites of pGC2.

DRWD FIG. 5. Antimicrobial susceptibility of various strains. The standard disk susceptibility procedure was used to test the antimicrobial susceptibility of RUSA315 (plate a), SWTD3 (plate b), COL (plate c), RUSA 12F (plate d), SWTD5 (plate e). Antibiotics: 1,. . .

DETD . . . fragments with the internal XbaI-HpaI fragment from Tn551 cloned into the plasmid pGEM-1 (plasmid pRT1, see Matthews and Tomasz, 1990, Antimicrob. Agents Chemother. 34:1777-79) to find positive fragments--there will be two if an enzyme that cuts Tn551 once is used. 3.. . .

DETD . . . mg/L methicillin to the medium resulted in a striking change in the composition of peptidoglycan (de Jonge and Tomasz, 1993, Antimicrobial. Agents and Chemotherapy, 37:342-6). In drug free medium, this bacterium produces a cell wall composed of a diverse family of. . .

DETD . . . stem peptide glutamic acid residues (see de Lencastre et al., 1994 "Molecular Aspects of Methicillin Resistance in Staphylococcus aureus", J. Antimicrob. Chemother. 33; de Jonge et al., 1992, J. Biol. Chem. 267:11255-9; Ornelas-Soares et al., 1993, J. Biol. Chem. 268:26268-72).

DETD . . . study
pGCSW-3)
SWTD3 COL.OMEGA.720 (femR315::Tn551) Em.sup.r This study
Mc.sup.r Cm.sup.r (RUSA315/pGCSW-3)
SWTD5 COL.OMEGA.558 (femD::Tn551) Em.sup.r Mc.sup.r This study
Cm.sup.r (RUSA12F/pGCSW-3)
Bacteriophage
Lambda DASH .RTM.II bh.degree. b189 KH54 chiC srl.degree. Stratagene
nin5 shndIII.degree. srl.degree.
red.sup.+ gam.sup.+
II/R315 Lambda DASH .RTM.II/15.5 kb EcoR1. . . (femR315 wild-type)

Mc.sup.r, methicillin resistance;
Em.sup.r, erythromycin resistance;
Amp.sup.r, ampicillin resistance;
Cm.sup.r, chloramphenicol resistance
References:
(1) de Lencastre and Tomasz, Antimicrob. Agents Chemother., 38:2590 (1994);
(2) Korblum et al., Eur. J. Clin. Microbiol., 5:714-718 (1986);
(3) BergerBachi et al., Antimicrob. Agents Chemother., 36:1367-1373 (1992);
(4) de Lencastre et al., J. Antimicrob. Chemother., 33:7-24 (1994);
(5) Matthews and Tomasz, Antimicrob. Agents Chemother., 34:1777-1779.

DETD . . . containing increasing concentrations of methicillin. CFU were determined after 48 h of incubation at 37.degree. C. [de Lencastre et al., Antimicrob Agents Chemother. 35:632-639 (1991)].

DETD . . . the insertional mutant RUSA315, is located on a 10.3 kb EcoR1 DNA fragment of the COL chromosome [DeLencastre and Tomasz, Antimicrob. Agents Chemother, 38:2590-2598 (1994)]. The approximately 15.5 kb EcoR1 fragment (which includes transposon Tn551) was isolated from strain RUSA315 and. . .

=> D BIB ABS L98 1

L98 ANSWER 1 OF 6 USPATFULL
AN 1999:67433 USPATFULL
TI Nucleic acid fragments, chimeric genes and methods for increasing the methionine content of the seeds of plants
IN Falco, Saverio Carl, Arden, DE, United States
Guida, Jr., Anthony Dominick, Newark, DE, United States
Locke, Mary Elizabeth Hartnett, Glassboro, NJ, United States
PA E. I. du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)
PI US 5912414 19990615
WO 9531554 19951123
AI US 1996-737524 19961108 (8)
WO 1995-US5545 19950512
19961108 PCT 371 date
19961108 PCT 102(e) date
RLI Continuation-in-part of Ser. No. US 1994-242408, filed on 13 May 1994, now abandoned
DT Utility
EXNAM Primary Examiner: Robinson, Douglas W.; Assistant Examiner: Nelson, Amy J.
CLMN Number of Claims: 37
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 2704
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Four chimeric genes are disclosed. A first chimeric gene encoding a plant cystathionine .gamma.-synthase (CS), a second chimeric gene encoding feedback-insensitive aspartokinase, which is operably linked to a plant chloroplast transit sequence, a third chimeric gene encoding bifunctional feedback-insensitive aspartokinase-homoserine dehydrogenase (AK-HDH), which is operably linked to a plant chloroplast transit sequence, and a fourth chimeric gene encoding a methionine-rich protein, all operably linked to plant seed-specific regulatory sequences are discussed. Methods for their use to produce increased levels of methionine in the seeds of transformed plants are provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> D KWIC

L98 ANSWER 1 OF 6 USPATFULL
DETD . . . of three adjacent nucleotides in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation). "Open reading frame" refers to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence.
DETD . . . the chloroplasts and therefore are synthesized with a chloroplast targeting signal. The plant-derived CS coding sequence includes the native chloroplast targeting signal, but bacterial proteins such as E. coli AKIII and AKII-HDHII have no such signal. A chloroplast transit sequence could, therefore, be fused to. . .
DETD The DNA insert in plasmid pFS1086 is 1048 bp in length and contains a long open reading frame and a poly A tail, indicating that it represents a corn cDNA. The deduced amino acid sequence of the open reading frame shows no similarity to the published sequence of E. coli CS [Duchange et al. (1983) J. Biol. Chem. 258:14868-14871]. None. . .
DETD . . . insert in plasmid pFS1088 is shown in SEQ ID NO:1. It is 1639 bp in length and contains a long open reading frame and a poly A tail, indicating that it too represents a corn cDNA. The deduced amino acid sequence of the open reading frame shows 59 percent similarity and 34 percent identity to the published sequence of E. coli CS (see FIG. 1), indicating. . .
DETD The open reading frame in plasmid pFS1088 continues to the 5' end of the insert DNA, and does not include an ATG initiator codon,. . . likely that most of the coding sequence, including a functional chloroplast targeting signal, is contained in the cloned insert. The open reading frame of pFS1088 is in frame with the initiator codon of the lacZ gene carried on the cloning vector. Thus, complementation. . .

DETD . . . corn CS gene the cDNA clone was used as a DNA hybridization probe to screen a genomic corn library. A genomic library of corn in bacteriophage lambda was purchased from Stratagene (La Jolla, Calif.). Data sheets from the supplier indicated that the corn DNA was from. . .

DETD . . . of the two DNA sequences 5' to the deletion region shows 88% identity. The deduced amino acid sequence of the open reading frame of the cDNA 3' to the deleted sequence shows 99.3% similarity and 98.9% identity when compared to the deduced amino. . .

DETD As indicated in Example 1, the open reading frame in plasmid pFS1088 for the corn CS gene does not include an ATG initiator codon. Oligonucleotide adaptors OTG145 and OTG146. . .

DETD A genomic library of corn in bacteriophage lambda was purchased from Clontech (Palo Alto, Calif.). Data sheets from the supplier indicated that the corn DNA was from. . .

DETD Plant amino acid biosynthetic enzymes are known to be localized in the chloroplasts and therefore are synthesized with a chloroplast targeting signal. Bacterial proteins such as AKIII have no such signal. A chloroplast transit sequence (cts) was therefore fused to the lsyC-M4 coding sequence. . .

DETD Plant amino acid biosynthetic enzymes are known to be localized in the chloroplasts and therefore are synthesized with a chloroplast targeting signal. Bacterial proteins have no such signal. A chloroplast transit sequence (cts) was therefore fused to the metL coding sequence in the chimeric. . .

=> D BIB ABS L98 2

L98 ANSWER 2 OF 6 USPATFULL
AN 1998:24926 USPATFULL
TI Vaccine for branhamelia catarrhalis
IN Murphy, Timothy F., East Amherst, NY, United States
PA Research Foundation of State University of New York, Amherst, NY, United States (U.S. corporation)
PI US 5725862 19980310
AI US 1995-569959 19951208 (8)
RLI Division of Ser. No. US 1994-306871, filed on 20 Sep 1994, now patented, Pat. No. US 5712118 which is a continuation-in-part of Ser. No. US 1993-129719, filed on 29 Sep 1993, now patented, Pat. No. US 5556755
DT Utility
EXNAM Primary Examiner: Minnifield, N. M.
LREP Hodgson, Russ, Andrews Woods & Goodyear
CLMN Number of Claims: 16
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 1877
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions comprising outer membrane protein "CD", and peptides and oligopeptides thereof, of Branhamella catarrhalis are described. Additionally, nucleotide sequences encoding the protein, peptide or oligopeptide are disclosed, as well as recombinant vectors containing these sequences. Protein, peptide or oligopeptide can be produced from host cell systems containing these recombinant vectors. Peptides and oligopeptides can also be chemically synthesized. Disclosed are the uses of the protein, peptides and oligopeptides as antigens for vaccine formulations, and as antigens in diagnostic immunoassays. The nucleotide sequences are useful for constructing vectors for use as vaccines for insertion into attenuated bacteria in constructing a recombinant bacterial vaccine, and for inserting into a viral vector in constructing a recombinant viral vaccine. Also described is the use of nucleotide sequences related to the gene encoding CD as primers and/or probes in molecular diagnostic assays for the detection of B. catarrhalis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> D KWIC 2

L98 ANSWER 2 OF 6 USPATFULL
DETD . . . CO.sub.2 or in brain heart infusion broth. Escherichia coli (E. coli) Y1090 was used as the host strain for the bacteriophage lambda gt11 genomic library. Depending on the circumstances, E. coli was grown in LB broth, or on LB agar containing 50 .mu.g/ml of. . .
DETD . . . the epitopes recognized by antibodies 7D6 and 5E8. Nucleotide sequence analysis of the insert contained within this clone showed an open reading frame with no start or stop codons (SEQ ID No. 1). The nucleotide sequence of this clone corresponds to nucleotides 775-1160. . .
DETD . . . synthesized to correspond to sequence at appropriate intervals within the insert such as represented by SEQ ID NOs. 2-13. An open reading frame of 453 amino acids, which represents a protein of 48,277 daltons, was identified (SEQ ID NO. 14). A strong transcriptional. . .
DETD . . . OMP CD observed in SDS-PAGE (60,000 or 55,000, daltons in reduced or nonreduced form, respectively). Therefore, a plasmid containing the open reading frame without downstream sequence was constructed to determine whether expression of the reading frame would yield a full size CD protein. A ClaI site is located 48 bp downstream of the open reading frame. A BamHI-ClaI DNA fragment of 1558 bp containing the putative CD gene was subcloned into pGEM7zf- (Promega Corp., Madison, Wis.). . .
DETD . . . acids being analyzed by a microsequencer. The amino terminal sequence, G-V-T-V-S-P-L-L-L-G corresponded to amino acids 27 through 36 of the open reading frame of pCD1, indicating that CD has a 26 amino acid leader peptide. A hydrophobic 26 amino acid leader peptide is. . .
DETD . . . was analyzed for the presence of methionine residues to predict the result of cyanogen bromide cleavage of the protein. The open

reading frame corresponding to the mature protein contains four methionines indicating that cleavage with cyanogen bromide would yield five fragments. Cyanogen bromide. . .

DETD Table 2 shows the size of the fragments (CD peptides) predicted by the methionine sites in the open reading frame . FIG. 6 shows the actual fragments obtained from cyanogen bromide treatment of purified CD, as determined by the tricine polyacrylamide. . .

DETD Thus, the open reading frame identified in pCD1 represents the entire gene encoding CD and the protein behaves aberrantly in SDS-PAGE. This discrepancy between the. . .

DETD In another illustration that the CD protein possesses properties desirable of a vaccine antigen, it was demonstrated that CD protein is the target of bactericidal antibody generated from immunization with CD protein. For example, polyclonal antiserum to CD protein was raised in a rabbit by. . . to 5.times.10.sup.4 colony forming units (CFU) per ml in 10% bovine serum albumin in a balanced salt solution. The bactericidal assay reaction contained bacteria, polyclonal antiserum to CD protein, a complement source consisting of normal human serum which was absorbed with protein G to remove antibodies, and the balanced. . .

CLM What is claimed is:

. . . mass of from 55,000 to 60,000 daltons by SDS-PAGE and which is encoded by a nucleotide sequence shown as an open reading frame in SEQ ID NO. 14; and (b) a physiological carrier.

=> D BIB ABS KWIC L98 3

L98 ANSWER 3 OF 6 USPATFULL
AN 1998:9349 USPATFULL
TI Vaccine for branhamella catarrhalis
IN Murphy, Timothy F., East Amherst, NY, United States
PA Research Foundation of State University of New York, Amherst, NY, United States (U.S. corporation)
PI US 5712118 19980127
AI US 1994-306871 19940920 (8)
RLI Continuation-in-part of Ser. No. US 1993-129719, filed on 29 Sep 1993, now patented, Pat. No. US 5556755, issued on 17 Sep 1996
DT Utility
EXNAM Primary Examiner: Hutzell, Paula K.; Assistant Examiner: Minnifield, N. M.
LREP Hodgson, Russ, Andrews, Woods & Goodyear
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 1838
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions comprising outer membrane protein "CD", and peptides and oligopeptides thereof, of Branhamella catarrhalis are described. Additionally, nucleotide sequences encoding the protein, peptide or oligopeptide are disclosed, as well as recombinant vectors containing these sequences. Protein, peptide or oligopeptide can be produced from host cell systems containing these recombinant vectors. Peptides and oligopeptides can also be chemically synthesized. Disclosed are the uses of the protein, peptides and oligopeptides as antigens for vaccine formulations, and as antigens in diagnostic immunoassays. The nucleotide sequences are useful for constructing vectors for use as vaccines for insertion into attenuated bacteria in constructing a recombinant bacterial vaccine, and for inserting into a viral vector in constructing a recombinant viral vaccine. Also described is the use of nucleotide sequences related to the gene encoding CD as primers and/or probes in molecular diagnostic assays for the detection of B. catarrhalis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
DETD . . . CO.sub.2 or in brain heart infusion broth. Escherichia coli (E. coli) Y1090 was used as the host strain for the bacteriophage lambda gt11 genomic library. Depending on the circumstances, E. coli was grown in LB broth, or on LB agar containing 50 .mu.g/ml of. . .
DETD . . . the epitopes recognized by antibodies 7D6 and 5E8. Nucleotide sequence analysis of the insert contained within this clone showed an open reading frame with no start or stop codons (SEQ ID No. 1). The nucleotide sequence of this clone corresponds to nucleotides 775-1160. . .
DETD . . . synthesized to correspond to sequence at appropriate intervals within the insert such as represented by SEQ ID NOs. 2-13. An open reading frame of 453 amino acids, which represents a protein of 48,277 daltons, was identified (SEQ ID NO. 14). A strong transcriptional. . .
DETD . . . OMP CD observed in SDS-PAGE (60,000 or 55,000, daltons in reduced or nonreduced form, respectively). Therefore, a plasmid containing the open reading frame without downstream sequence was constructed to determine whether expression of the reading frame would yield a full size CD protein. A ClaI site is located 48 bp downstream of the open reading frame. A BamHI-ClaI DNA fragment of 1558 bp containing the putative CD gene was subcloned into pGEM7zf- (Promega Corp., Madison, Wis.). . .
DETD . . . acids being analyzed by a microsequencer. The amino terminal sequence, G-V-T-V-S-P-L-L-L-G corresponded to amino acids 27 through 36 of the open reading frame of pCD1, indicating that CD has a 26 amino acid leader peptide. A hydrophobic 26 amino acid leader peptide is. . .
DETD . . . was analyzed for the presence of methionine residues to predict the result of cyanogen bromide cleavage of the protein. The open reading frame corresponding to the mature protein contains four methionines indicating that cleavage with cyanogen bromide would yield five fragments. Cyanogen bromide. . .
DETD Table 2 shows the size of the fragments (CD peptides) predicted by the methionine sites in the open reading frame . FIG. 6 shows the actual fragments obtained from cyanogen bromide

treatment of purified CD, as determined by the tricine polyacrylamide. . . .

DETD Thus, the open reading frame identified in pCD1 represents the entire gene encoding CD and the protein behaves aberrantly in SDS-PAGE. This discrepancy between the. . .

DETD In another illustration that the CD protein possesses properties desirable of a vaccine antigen, it was demonstrated that CD protein is the target of bactericidal antibody generated from immunization with CD protein. For example, polyclonal antiserum to CD protein was raised in a rabbit by. . . to 5.times.10.sup.4 colony forming units (CFU) per ml in 10% bovine serum albumin in a balanced salt solution. The bactericidal assay reaction contained bacteria, polyclonal antiserum to CD protein, a complement source consisting of normal human serum which was absorbed with protein G to remove antibodies, and the balanced. . .

CLM What is claimed is:

. . . 5. An isolated nucleic acid molecule selected from the group consisting of a gene depicted as a 1359 base pair open reading frame of SEQ ID No. 14, and a fragment of said gene, wherein said fragment encodes at least one epitope of. . .

=> D BIB ABS KWIC L98 4

L98 ANSWER 4 OF 6 USPATFULL
AN 97:107218 USPATFULL
TI Vesicle membrane transport proteins
IN Edwards, Robert H., Los Angeles, CA, United States
PA The Regents of the University of California, Oakland, CA, United States (U.S. corporation)
PI US 5688936 19971118
AI US 1993-63552 19930514 (8)
RLI Continuation-in-part of Ser. No. US 1992-923096, filed on 30 Jul 1992, now abandoned which is a continuation-in-part of Ser. No. US 1992-899074, filed on 11 Jun 1992, now abandoned
DT Utility
EXNAM Primary Examiner: Zitomer, Stephanie W.
LREP Merchant, Gould, Smith, Edell, Welter & Schmidt
CLMN Number of Claims: 1
ECL Exemplary Claim: 1
DRWN 65 Drawing Figure(s); 52 Drawing Page(s)
LN.CNT 3377
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Complete cDNA and amino acid sequences are disclosed for rat adrenal-specific and brain-specific transport protein, as well as for human brain-specific transport protein. Methods for obtaining the genes encoding these proteins and for obtaining recombinantly produced protein are described. Antibodies and methods for isolating additional vesicle membrane transport proteins are also described. Methods for using the vesicle membrane transport proteins to identify compounds that selectively inhibit transport of toxic molecules into vesicles, and that prevent inhibition of transport of toxic molecules are also provided. The invention includes methods to treat and diagnose diseases associated with sequestration of toxic molecules in mammalian cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
DETD Genomic DNA in a .lambda. bacteriophage vector library was also used to isolate substantially purified DNA comprising the gene for hSVAT, including the introns originally present. . .
DETD In another embodiment, as discussed below in Example 3, a probe specific for the DNA encoding CGAT protein was used to screen a bacteriophage .lambda.gt10 rat brainstem cDNA library. Sequencing of the resulting clones resulted in the determination of the nucleotide sequence and protein. . .
DETD . . . 2.5 kb insert. Sequence analysis of this insert showed that the first ATG occurred at the beginning of the largest open reading frame, in a context that conforms to the consensus for translation initiation (FIG. 1) (SEQ ID NO: 1) (Kozak, Nucl. Acids.. . .

=> D BIB ABS KWIC L98 5

L98 ANSWER 5 OF 6 USPATFULL
AN 97:63871 USPATFULL
TI Method of detecting compounds utilizing genetically modified lambdoid bacteriophage
IN Ray, Bryan L., Burlington, MA, United States
Lin, Edmund C. C., Boston, MA, United States
Crea, Roberto, San Mateo, CA, United States
PA SymBioTech, Inc., Woburn, MA, United States (U.S. corporation)
PI US 5650267 19970722
AI US 1994-299249 19940831 (8)
RLI Continuation of Ser. No. US 1993-53865, filed on 27 Apr 1993, now abandoned
DT Utility
EXNAM Primary Examiner: Fleisher, Mindy; Assistant Examiner: McKelvey, Terry A.
LREP Hale and Dorr LLP
CLMN Number of Claims: 32
ECL Exemplary Claim: 1
DRWN 16 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1246
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is an infective lambdoid bacteriophage which includes a protein construct comprising a genetically modified major tail protein truncated at its carboxy terminus, and a target molecule peptide bonded to the carboxy terminus of the tail protein. Also disclosed are nucleic acids encoding the construct and methods of detecting a molecule-of-interest in a solution and of detecting a cell which produces a molecule-of-interest.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
SUMM . . . to express lambdoid components and the protein construct, and then to assemble a lambdoid phage therefrom, the phage having the target protein on its outer surface. The bacteriophage are then isolated from the cell.
DETD . . . bacterial strains results from the presence of a molecule-of-interest in the solution-to-be-tested depending on the nature of the infecting lambdoid bacteriophage genome and any specific needs of the infected bacteria. This method has also been adapted to select or screen for cell. . .
DETD . . . a flexible tail 150 nm long ending in a tapered basal part and a single tail fiber (FIG. 1A). The genome of the bacteriophage is linear DNA. This DNA is found in the capsid head and has cohesive ends, the right one of which. . .
DETD . . . the beginning of the CNTF coding region is necessary to keep the V gene and CNTF gene in the same open reading frame so that the two genes will be translated into a single polypeptide. This specific dinucleotide was chosen so as to. . .

=> D BIB ABS KWIC L98 6

L98 ANSWER 6 OF 6 USPATFULL
AN 97:59092 USPATFULL
TI Method for isolating mutant cells
IN Ray, Bryan L., Burlington, MA, United States
Lin, Edmund C. C., Boston, MA, United States
Crea, Roberto, San Mateo, CA, United States
PA President and Fellows of Harvard College, Cambridge, MA, United States (U.S. corporation)
PI US 5646030 19970708
AI US 1994-294386 19940823 (8)
RLI Continuation-in-part of Ser. No. US 1992-991115, filed on 16 Dec 1992, now patented, Pat. No. US 5348872 which is a continuation-in-part of Ser. No. US 1992-856876, filed on 24 Mar 1992, now abandoned which is a continuation of Ser. No. US 1990-541895, filed on 21 Jun 1990, now abandoned
DT Utility
EXNAM Primary Examiner: Walsh, Stephen G.; Assistant Examiner: Sorensen, Kenneth A.
LREP Lappin & Kusmer LLP
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 19 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 1869
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for isolating a mutant cell that excretes a desired compound. The method includes culturing a plurality of auxotrophic pretreated starter cells and auxotrophic feeder cells in the presence of a reversibly noninfective, modified lambdoid bacteriophage. If the treated starter cell produces the desired compound, the bacteriophage will be rendered infective and infect the feeder cell. The feeder cell, in turn, will excrete a metabolite required by the starter cell and the starter cell will excrete a metabolite required by the feeder cell, enabling the cells to cross-feed, grow, and produce a colony containing a starter cell which produces the desired compound.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
SUMM The lambdoid **bacteriophage** includes a modified gpV **protein** to which a target protein is linked. As used herein the term "gpV protein" is meant to encompass any major tail protein found in. . .
DETD . . . a flexible tail 150 nm long ending in a tapered basal part and a single tail fiber (FIG. 1A). The **genome** of the **bacteriophage** is linear DNA. This DNA is found in the capsid head and has cohesive ends, the right one of which. . .
DETD . . . metabolite, which the feeder bacteria requires for growth. Additionally, the feeder cell requires for growth a gene present in the **bacteriophage genome**. In this method, the **bacteriophage** has a temperature sensitive genotype (e.g., CIts 857) and carries a selectable marker gene may be employed to infect a. . . matrix or receptor. If an enzyme-producing cell is present, the enzyme produced by the treated starter cell cleaves the bound, **bacteriophage**-linked **target protein**, thereby releasing the **bacteriophage** and rendering it infective again. The released bacteriophage then infects the feeder cell at low growth temperature, providing it with. . .
DETD . . . the beginning of the CNTF coding region is necessary to keep the V gene and CNTF gene in the same **open reading frame** so that the two genes will be translated into a single polypeptide. This specific dinucleotide was chosen so as to. . .